

Figure 2

A

Igα-1S (sense oligo for Igα containing and SpeI and HindIII cloning sites)
5' TAG TGA ACT AGT AAG CTT GCC ACC ATG CCA GGG GGT CTA GAA GCC CTC A
3'

Igα-221A (antisense oligo for Igα containing EcoRI and ClaI cloning sites)
5' GTC TAG ATC GAT GAA TTC TCA TGG CTT TTC CAG CTG GGC ATC 3'

Igβ-1S (sense oligo for Igβ containing SpeI and HindIII cloning sites)

5' TAG TGA ACT AGT AAG CTT GCC ACC ATG GCC ACA CTG GTG CTG TCT TCC
ATG 3'

IgB-229A (antisense oligo for Igβ containing XhoI and ClaI cloning sites)
3 GTC TAG ATC GAT CTC GAG TCA TTC CTG GCC TGG ATG CTC TCC TAC CGA 3'

↓**3B.** ||⊔

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1,3

13

MW ---PCR--- MW Stds Igα Igβ Stds



~700 bp-

Figure 3

p3.1NeoIg_ Length: 681

Translation

HindIII Signal M P G G L E A L R A L P L

AAGCIT GOCACC AIG CCA GGG GGT CIA GAA GCC CIC AGA GCC CIG CCT CIC

L L F L S Y A C L G P G C Q A L R CTC CTC TTC TTG TCA TAC GCC TGT TTG GGT CCC GGA TGC CAG GCC CTG CGG

V E G G P P S L T V N L G E E A R GIA GAA GOG GOT CCA CCA TOC CIG ACG GIG AAC TIG GOC GAG GAG GCC CCC

L T C E N N G R N P N I T W W F S CIC ACC TGT GAA AAC AAT GOC AGG AAC CCT AAT ATC ACA TGG TGG TTC AGC

L Q S N I T W P P V P L G P G Q G

T T G Q L F F P E V N K N H R G L ACC ACA COC CAA GIA AAC AAG AAC CAC AGG CGC TIG \overline{A}

Y W C Q V I E N N I L K R S C G T TAC TOG TOC CAA GIG ATA GAA AAC AAC ATA TTA AAA COC TOC TOT GOT ACT

Y L R V R N P V P R P F L D M G E TAC CTC CCC GTG CCC AAT CCA GTC CCT AGG CCC TTC CTG GAC ATG GGG GAA

G T K N R I I T A E G I I L L F C
GGT ACC AAG AAC CGC ATC ATC ACA GCA GCA GGG ATC ATC TIG CIG TIC TGT

A V V P G T L L F R K R W Q N E GCA GIG GIG CCA GCG CAG CCG CIG CIG CIG ACG AAA CCG TCG CAA AAT CAG

K F G V D M P D D Y E D E N L Y E AAG TIT COG CIIG CAC AIG CCA GAT CAC TAT, CAA CAT CAA AAT CIC TAT CAG

G L N L D D C S M Y E D I S R G L \bigcirc GCC CTG AAC CTT CAT CAC TGT TCT ATG TAT CAG CAC ATC TCC ACG CCA CTC

Q G T Y Q D V G N L H I G D A Q L CAG GGC ACC TAC CAG GAT GIG GGC AAC CTC CAC ATT GGA GAT GCC CAG CTG

E K P * FCORI GAA AAG CCA TGA GAATTC

Figure 4

p3.1zeoIg_ Length: 705

Translation

HindIII Signal M A T L V L S S M P C H W

AACCIT GCCACC AIG GCC ACA CIG GIG CIG TCT TCC AIG CCC TGC CAC TGG

L L F L L L F S G E P V P A M T CIG TIG TIC CIG CIG CIG CIC TIC TCA GGT GAG COG GITA CCA GCA ATG ACA

S S D L P L N F Q G S P C S Q I W AGC AGT GAC CTG CCA CTG AAT TIC CAA GCA AGC CCT TGT TCC CAG ATC TGG

Q H P R F A A K K R S S M V K F H CAG CAC COG AGG TIT GCA GCC AAA AAG COG AGC TOC ATG GTG AAG TIT CAC

C Y T N H S G A L T W F R K R G S TOC TAC ACA AAC CAC TOA GGT GCA CTG ACC TGG TTC CGA AAG CGA GGG AGC

UNGSVYTLTIQNIQYEDN DAAT GGC TCT GTC TAC ACC CTC ACT ATC CAA AAC ATC CAG TAC GAG GAT AAT

GET ATC TAC TIC TOC AAG CAG AAA TGT GAC AGC GOC AAC CAT AAT GIC ACC

D S C G T E L L V L G F S T L D Q GAC AGC TET GOC ACG CAA CIT CITA GIC TITA GGA TIC AGC ACG TIG GAC CAA

L K R R N T L K D G I I L I Q T L CTG AAG COG COG AAC ACA CTG AAA GAT GOC ATT ATC TTG ATC CAG ACC CTC

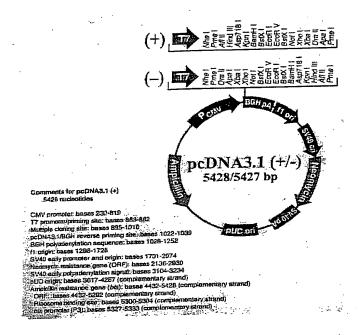
D G K A G M E E D H T Y E G L N I GAC GGC AAG GCT GGG ATG GAG GAA GAT CAC ACC TAT GAG GGC TTG AAC ATT

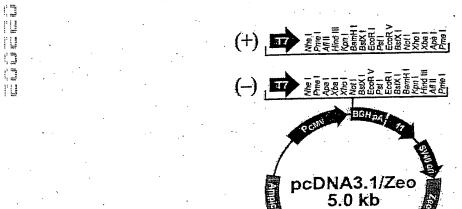
D Q T A T Y E D I V T L R T G E V GAC CAG ACA GOC ACC TAT GAA GAC ATA GIG ACT CIT COG ACA GOG GAG GIA

K W S V G E H P G Q E \star XhoI AAG TGG TGG GI'A GGA GAG CAT CCA GGC CAG GAA TGA CTCGAG

Figure 5

U D Figure 6

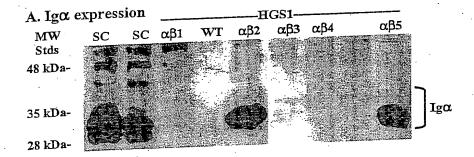




Comments for peDNA3.1/Zeo (+) .5015 auclientides

CMV promoter, hases 209-863
T7 promoter, priming site: hases 863-882
Multiple cloning site: bases 895-1010
BCH reverse priming site: bases 1022-1039
BCH polyadenylation signal; bases 1021-1235
H origin; bases 1298-1211
SV40 promoter and origin; bases 1776-2101
EM7 promoter; bases 2177-2183
Zeocin; resistance gene: bases 2184-2558
SV40 polyadenylation; bases 2184-2558
SV40 polyadenylation; bases 2688-2827
BUILC origin; bases 2201-3874 (C)
Bio promoter; bases 4880-4978 (C)
Ampicillin (bla) resistance gene: bases 4019-1879 (C)

Figure 7:



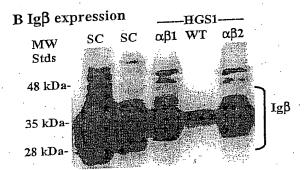


Figure 8

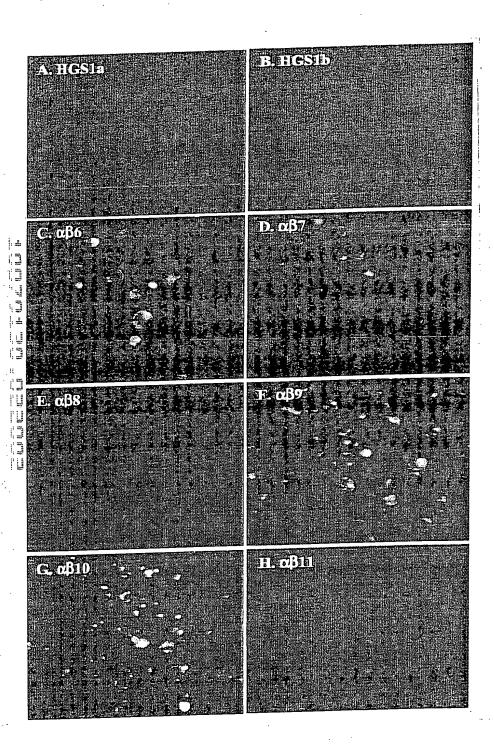


Figure 8 (continued)

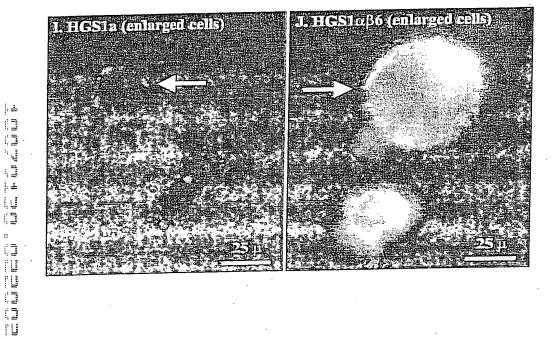
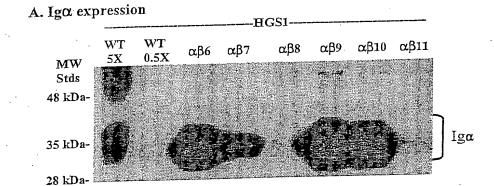
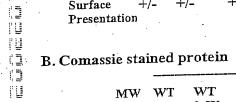


Figure 9





Surface

Presentation

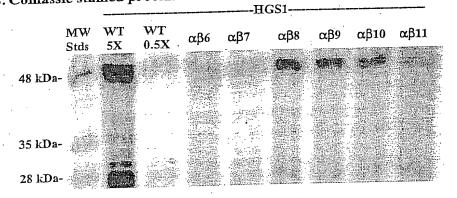


Figure 10

P 1.5 2. C. 1.9 P

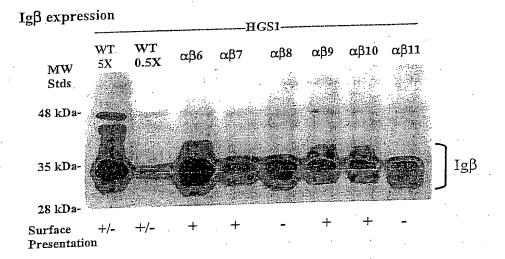
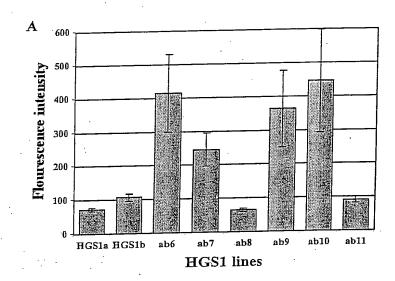


Figure 11



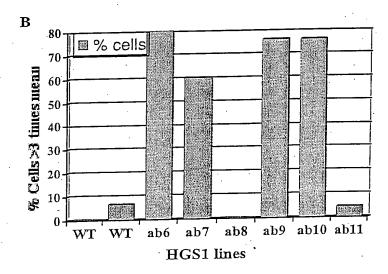
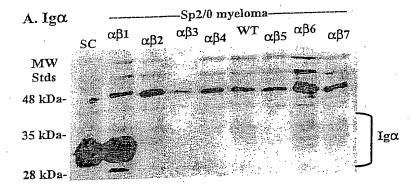


Figure 12



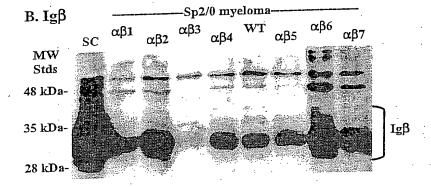


Figure 13

North (Last Control of the Control o

